

PW248 Enrichment and characterization of microorganisms capable of degrading various C1 compounds in the Black Sea

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Background: Methylated compounds can be used as an energy source to drive interactions between sulfate reducing microorganisms and methanogens. This has potential impact on the current understanding of the global carbon and sulfur cycles.

Objectives: The use of methylated compounds by anaerobic microorganisms present in the sulfidic permanently stratified Black Sea sediment and column water and the composition of these communities was investigated through enrichment studies.

Methods: Black Sea sediment of three different depths between 5 and 30 centimeters below sea floor, as well as water at 105 meters deep were collected anoxically and used for enrichments, supplemented with 1 mM of either dimethylsulfide (DMS), dimethylsulfoniopropionate (DMSP), trimethylamine (TMA) and methanol as sole energy source. To promote methanogenesis, acetogenesis and sulfate reduction in the different enrichments, 20 mM molybdate, 20 mM bromoethanesulfonate (BrES) and 20 mM BrES with 20 mM sulfate was added, respectively. Anoxic cultures were incubated at 20°C in the dark. Uptake of substrate and product formation were monitored over 4 weeks. Active cultures were transferred to fresh medium to promote further enrichment. Analyses of 16s rRNA gene sequencing are ongoing to elucidate the inocula and culture communities.

Results: All enrichments grew on the provided substrates. Over four weeks, utilization of substrate ranged between 20% and 100% for all enrichments. Subsequent transfers of the enrichments retained the decrease of substrate although utilization was slower. These results will be complemented with 16s rRNA gene sequencing data and community comparison developed in methanogenic, acetogenic and sulfate-reducing enrichments performed.